

SEP 16 2003

TECH CEN



1600

## RAW SEQUENCE LISTING

DATE: 09/11/2003

PATENT APPLICATION: US/09/973,382C

TIME: 11:29:04

Input Set : A:\D6230SEQ.txt

Output Set: N:\CRF4\09112003\I973382C.raw

2 <110> APPLICANT: Heston, Warren D.W.  
3 O'Keefe, Denise S.  
5 <120> TITLE OF INVENTION: DNA Encoding the Prostate-Specific Membrane  
6 Antigen-Like Gene and Uses Thereof  
8 <130> FILE REFERENCE: D6230  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/973,382C  
11 <141> CURRENT FILING DATE: 2001-10-09  
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/09417  
14 <151> PRIOR FILING DATE: 2000-04-09  
16 <160> NUMBER OF SEQ ID NOS: 38  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1992  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
23 <220> FEATURE:  
24 <223> OTHER INFORMATION: cDNA sequence of PSMA-like gene  
26 <400> SEQUENCE: 1  
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28 aggattttta gagcttatag tagcaaaaag aaaagggaaa ttctctctga 100  
29 gatgtccttt ttgtaggcc taatgacaaa aggttgaaga taaagttcta 150  
30 gtactcattt aagtgttaata ttgaaaattg atattaccaa atctggaaca 200  
31 accaatttta aataaggaaa gaaagacact gtgttttcta ggtaaaaaat 250  
32 gccagctgg caggggccaa aggagtcatt ctctactcag accctgctga 300  
33 ctactttgct cctgggggtga agtcctatcc agacggttgg aatcttctg 350  
34 gaggtggtgt ccagcgtgga aatataccta atctgaatgg tgcaggagac 400  
35 cctctcacac caggttaccc agcaaatgaa tacgcttata ggcattggaat 450  
36 tgcagaggct gttggtcttc caagtattcc tgttcatcca gttggatact 500  
37 atgatgcaca gaagtccta gaaaaaatgg gtggctcagc accaccagat 550  
38 agcagctgga gaggaagtct caaagtgtcc tacaatgttg gacctggctt 600  
39 tactggaaac ttttctacac aaaaagtcaa gatgcacatc cactctacca 650  
40 atgaagtgac gagaatttac aatgtgatag gtactctcag aggagcagtg 700  
41 gaaccagaca gatatgtcat tctgggaggt caccgggact catgggtggt 750  
42 tgggtggtatt gaccctcaga gtggagcagc tgttggtcat gaaactgtga 800  
43 ggagctttgg aacactgaaa aaggaagggt ggagacctag aagaacaatt 850  
44 ttgtttgcaa gctgggatgc agaagaattt ggtcttcttg gttctactga 900  
45 gtgggcagag gataattcaa gactccttca agagcgtggc gtggcttata 950  
46 ttaatgtcga ctcatctata gaaggaaact acactctgag agttgattgt 1000  
47 acaccactga tgtacagctt ggtatacaac ctaacaaaag agctgaaaag 1050  
48 ccctgatgaa ggctttgaag gcaaatctct ttatgaaagt tggactaaaa 1100  
49 aaagtccttc ccagagttc agtggcatgc ccaggataag caaattggga 1150  
50 tctggaaatg attttgaggt gttcttccaa cgacttgga ttgcttcagg 1200  
51 cagagcacgg tatactaaaa attgggaaac aaacaaattc agcggctatc 1250  
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55 atgctgtagt ttttaagaaag tatgctgaca aaatctacaa tatttctatg 1450
56 aaacatccac aggaaatgaa gacatacagt ttatcatttg attcactttt 1500
57 ttctgcagta aaaaatttta cagaaattgc ttccaagttc agcgagagac 1550
58 tccaggactt tgacaaaagc aaccaatat tgtaagaat gatgaatgat 1600
59 caactcatgt ttctggaaag agcatttatt gatccattag ggttaccaga 1650
60 cagacctttt tataggcatg tcatctatgc tccaagcagc cacaacaagt 1700
61 atgcagggga gtcattccca ggaatttatg atgctctgtt tgatattgaa 1750
62 agcaaagtgg acccttccca ggcctgggga gatgtgaaga gacagatttc 1800
63 tgttgacaggc ttcacagtgc aggcagctgc agagactttg agtgaagtag 1850
64 cctaagagga ttctttagag actctgtatt gaatttgtgt ggtatgtcac 1900
65 tcaaagaata ataatgggta tattgataaa ttttaaaatt ggtatatttg 1950
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70 <211> LENGTH: 442
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <220> FEATURE:
75 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA-like
76 protein
78 <400> SEQUENCE: 2
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81 Lys Val Ser Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser
82 20 25 30
83 Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
84 35 40 45
85 Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
86 50 55 60
87 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
88 65 70 75
89 Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
90 80 85 90
91 Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
92 95 100 105
93 Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
94 110 115 120
95 Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
96 125 130 135
97 Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
98 140 145 150
99 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu
100 155 160 165
101 Val Tyr Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe
102 170 175 180
103 Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser
104 185 190 195
105 Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly

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106	200	205	210
107 Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly			
108	215	220	225
109 Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly			
110	230	235	240
111 Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu			
112	245	250	255
113 Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln			
114	260	265	270
115 Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu			
116	275	280	285
117 Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala			
118	290	295	300
119 Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys			
120	305	310	315
121 Thr Tyr Ser Leu Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn			
122	320	325	330
123 Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe			
124	335	340	345
125 Asp Lys Ser Asn Pro Ile Leu Leu Arg Met Met Asn Asp Gln Leu			
126	350	355	360
127 Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp			
128	365	370	375
129 Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn			
130	380	385	390
132 Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe			
133	395	400	405
134 Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val			
135	410	415	420
136 Lys Arg Gln Ile Ser Val Ala Ala Phe Thr Val Gln Ala Ala Ala			
137	425	430	435
138 Glu Thr Leu Ser Glu Val Ala			
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142 &lt;210&gt; SEQ ID NO: 3

143 &lt;211&gt; LENGTH: 2653

144 &lt;212&gt; TYPE: DNA

145 &lt;213&gt; ORGANISM: Homo sapiens

147 &lt;220&gt; FEATURE:

148 &lt;223&gt; OTHER INFORMATION: nucleotide sequence of human PSMA gene

150 &lt;300&gt; PUBLICATION INFORMATION:

151 &lt;308&gt; DATABASE ACCESSION NO: GenBank Accession No. M99487

152 &lt;309&gt; DATABASE ENTRY DATE: 1995-01-08

154 &lt;400&gt; SEQUENCE: 3

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156 tctcgctcgg attggttcag tgcactctag aaacactgct gtggtggaga	100
157 aactggaccc caggtctgga gcgaattcca gcctgcaggg ctgataagcg	150
158 aggcattagt gagattgaga gagactttac cccgccgtgg tggttggagg	200
159 gcgcgcagta gagcagcagc acaggcgcgg gtcccgggag gccggctctg	250
160 ctcgcgccga gatgtggaat ctccttcacg aaaccgactc ggctgtggcc	300

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163 atgaagctac taacattact ccaaagcata atatgaaagc atttttggat 450
164 gaattgaaag ctgagaacat caagaagttc ttatataatt ttacacagat 500
165 accacattta gcaggaacag aacaaaactt tcagcttgca aagcaaattc 550
166 aatcccagtg gaaagaattt ggcctggatt ctgttgagct agcacattat 600
167 gatgtcctgt tgcctaccc aaataagact catcccaact acatctcaat 650
168 aattaatgaa gatggaaatg agattttcaa cacatcatta tttgaaccac 700
169 ctctccaggt atatgaaaat gtttcggata ttgtaccacc tttcagtgct 750
170 ttctctcctc aaggaatgcc agaggcgat ctagtgtatg ttaactatgc 800
171 acgaactgaa gacttcttta aattggaacg ggacatgaaa atcaattgct 850
172 ctgggaaaat tgtaattgcc agatatggga aagttttcag aggaaataag 900
173 gttaaaaatg ccagctggc aggggccaaa ggagtcattc tctactccga 950
174 ccctgctgac tactttgctc ctggggtgaa gtcctatcca gatggttgga 1000
175 atcttcctgg aggtggtgtc cagcgtggaa atatcctaaa tctgaatggt 1050
176 gcaggagacc ctctcacacc aggttaccca gcaaatgaat atgcttatag 1100
177 gcgtggaatt gcagaggctg ttggtcttcc aagtattcct gttcatccaa 1150
178 ttggatacta tgatgcacag aagctcctag aaaaaatggg tggctcagca 1200
179 ccaccagata gcagctggag aggaagtctc aaagtgcct acaatgttg 1250
180 acctggcttt actggaaact tttctacaca aaaagtcaag atgcacatcc 1300
181 actctaccaa tgaagtgaca agaatttaca atgtgatagg tactctcaga 1350
182 ggagcagtg aaccagacag atatgtcatt ctgggaggtc accgggactc 1400
183 atgggtgttt ggtggtattg accctcagag tggagcagct gttgttcatg 1450
184 aaattgtgag gagctttgga aactgaaaa aggaaggggt gagacctaga 1500
185 agaacaattt tgtttgcaag ctgggatgca gaagaatttg gtcttcttgg 1550
186 ttctactgag tgggcagagg agaattcaag actccttcaa gagcgtggcg 1600
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188 gttgattgta caccgctgat gtacagcttg gtacacaacc taacaaaaga 1700
189 gctgaaaagc cctgatgaag gctttgaagg caaatctctt tatgaaagtt 1750
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191 aaattgggat ctggaaatga ttttgaggtg ttcttccaac gacttggaat 1850
192 tgcttcaggc agagcacggt atactaaaaa ttgggaaaca aacaaattca 1900
193 gcggctatcc actgtatcac agtgtctatg aaacatatga gttggtggaa 1950
194 aagttttatg atccaatgtt taaatatcac ctactgttg cccaggttcg 2000
195 aggagggatg gtgtttgagc tagccaattc catagtgtct ccttttgatt 2050
196 gtcgagatta tgctgtagtt ttaagaaagt atgctgacaa aatctacagt 2100
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198 ttcaactttt tctgcagtaa agaattttac agaaattgct tccaagttca 2200
199 gtgagagact ccaggacttt gacaaaagca acccaatagt attaagaatg 2250
200 atgaatgata aactcatggt tctggaaaga gcatttattg atccattagg 2300
201 gttaccagac aggccttttt ataggcatgt catctatgct ccaagcagcc 2350
202 acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
203 gatattgaaa gcaaatggga cccttccaag gcctggggag aagtgaagag 2450
204 acagatttat gttgcagcct tcacagtgca ggcagctgca gagactttga 2500
205 gtgaagttag ctaagaggat tctttagaga atccgtattg aatttgtgtg 2550
206 gtatgtcact cagaaagaat cgtaatgggt atattgataa attttaaaat 2600
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208 aaa 2653
211 <210> SEQ ID NO: 4

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Input Set : A:\D6230SEQ.txt

Output Set: N:\CRF4\09112003\I973382C.raw

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212 <211> LENGTH: 750
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA protein
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224 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
225                               35          40          45
226 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
227                               50          55          60
228 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr
229                               65          70          75
230 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
231                               80          85          90
232 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
233                               95         100         105
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235                               110        115        120
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237                               125        130        135
238 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
239                               140        145        150
240 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
241                               155        160        165
242 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
243                               170        175        180
244 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
245                               185        190        195
246 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
247                               200        205        210
248 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val
249                               215        220        225
250 Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
251                               230        235        240
252 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg
253                               245        250        255
254 Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro
255                               260        265        270
256 Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu
257                               275        280        285
258 Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr
259                               290        295        300
260 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro
261                               305        310        315
263 Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly

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VERIFICATION SUMMARY

DATE: 09/11/2003

PATENT APPLICATION: US/09/973,382C

TIME: 11:29:05

Input Set : A:\D6230SEQ.txt

Output Set: N:\CRF4\09112003\I973382C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number